



# SEQUENCE LISTING

<110> Terek, Richard M.

<120> CHONDROSARCOMA ASSOCIATED GENES

<130> 21486-021DIV

<140> US 09/819,144

<141> 2001-03-27

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 164

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(156)

<400> 1

atg gct gcg ggt ccc agg cca gga gct ccc tgc agg gcg ggg gct ccc	48
Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro	
1 5 10 15	

acg atc gta ttg acc tct gga aga aga cag aca ctt tcc cac ggg agc	96
Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser	
20 25 30	

tcc tct cca gcc aga gct aca ctt ggc aaa cct ttg gtc cta aat gat	144
Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp	
35 40 45	

tat tca ctg aat tgaagaaa	164
Tyr Ser Leu Asn	
50	

<210> 2

<211> 52

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro	
1 5 10 15	
Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser	
20 25 30	
Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp	
35 40 45	
Tyr Ser Leu Asn	
50	

<210> 3  
 <211> 884  
 <212> DNA  
 <213> Homo sapiens

<400> 3

acttccctgg	gttcacagca	ggggtggaac	tggattcttc	ctggatgggg	atccagatgg	60
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gggcgggggc	tcccacgac	gtattgacct	ctggaagaag	acagacactt	tcccacggga	180
gctcctctcc	agccagagct	acacttggca	aacctttggt	cctaaatgat	tattcactga	240
attgaagaaa	tacggtttac	atatcttcca	agtatatatg	tagggttgat	ttgggaagca	300
gaacacagca	gcccaaattt	gcttgtaatg	tctgcgacta	cagcctgctg	gcctgccttc	360
actgtcttgg	gggaagctcg	gggagaccag	gtggactgga	gtagactgtg	cagagacact	420
ggtctggtga	agatgtccag	gaaaccacga	gcctccagcc	cattttccaa	caaccaccca	480
tcaacaccaa	agaggttccc	aagacaaccc	agaagggaaa	agggaccctg	caaggaagtt	540
ccaggaacaa	aaggctctcc	ctaaaagacc	accgcttcaa	aaaaacctga	ggaatggagt	600
gggccaacac	tatccagcca	ctctgaccag	ccgaacgagg	aactcaatca	aaatgcgcca	660
tagcaggacc	acaagggcaa	ggagaccacc	gccttctcca	gtgcttcctt	gggcagccag	720
taattcccag	gcaaggccag	agacttcaag	tctatctgaa	aagtctccag	aagtctaacc	780
ccagataaat	agccaacagg	gtgtagagta	cgttttacac	ccaaagggta	atgccccatg	840
gtgatggaaa	taaaatgaac	atgttgtaaa	atgaaaaaaa	aaaa		884

<210> 4  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial sequence: oligonucleotide primer

<220>  
 <221> misc\_feature  
 <222> (1)...(14)  
 <223> n = A,T,C or G

<400> 4  
 tttttttttt ttvn 14

<210> 5  
 <211> 1946  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1946)  
 <223> n = A,T,C or G

<400> 5

cacgcaaagc	agtgtggggt	gattctgagg	tgcactgtgg	gaaagagctt	gtcgctgcgg	60
tgttgctgtt	ggagactcga	ttgttggtga	cagcgaaaga	acgataacaa	aatgccggag	120
cgagatagtg	agccgttctc	caaccctttg	gcccccgatg	gccacgatgt	ggatgatcct	180
cactccttcc	accaatcaaa	actcaccaat	gaagacttca	ggaaantnnt	catgaccccc	240
agggntgcac	ntacntntgc	accacnttnt	aantnnnntc	accatgagat	gccaagggag	300
tacaatgagg	atgaagaccc	agctgcacga	aggaggaaaa	agaaaagtta	ttatgccaag	360
ctacgccaac	aagaaattga	gagagagaga	gagctagcag	agaagtaccg	ggatcgtgcc	420

aaggaacgga	gagatggagt	gaacaaagat	tatgaagaaa	ccgagcttat	cagcaccaca	480
gctaactata	gggctgttgg	ccccactgct	gaggcggaca	aatcagctrc	agnnragaga	540
agacanwnda	hcnaggagtc	caaattcttg	ggtggtgaca	tggaaacacac	ccatttggtg	600
aaaggcttgg	attttgntnt	gcttchnaan	gtncgagctg	agattgncms	cmnanaraaa	660
nargaarang	nnctgatggn	aaancccmg	aaagaaacca	agaaagatga	ggatcctgaa	720
aataaaattg	aatttaaaac	acgtctgggc	cgcaatgttt	accgaatgct	ttttaagagc	780
aaagcatatg	agcggaatga	gttggttcctg	ccgggcccga	tggcctatgt	ggtagacctg	840
gatgatgagt	atgctgacac	agatatcccc	accactctta	tcccgcagca	aggctgattg	900
ccccaccatg	gaggcccaga	ccacactgac	cacaaatgac	attgtcatta	gcaagctgac	960
ccagatcctt	tcatacctga	ggcagggaaac	ccgtaacaag	aagcttaaga	agaaggataa	1020
agggaagccg	gaagagaaga	aacctcctga	ggctgacatg	aatatTTTTg	aagacattgg	1080
ggattacgta	ccctccacaa	ccaagacacc	tcgggacaag	gagcgggaga	gatatcggga	1140
acgggagcgt	gatcgggaaa	gagacagaga	ccgtgaccga	gagcgagagc	gagaacgaga	1200
tcgggaacga	gagcgagagc	gggaccgaga	gagagaagag	gaaaagaaga	gacacagcta	1260
ctttgagaag	ccaaaagtag	atgatgagcc	catggacgtt	gacaaaggac	ctgggtctac	1320
caaggagttg	atcaagtcca	tcaatgaaaa	gtttgctggg	tctgctggct	gggaaggcac	1380
agaatcgctg	aagaagccag	aagacaaaaa	gcagctggga	gatttctttg	gcatgtccaa	1440
cagttatgca	gagtgtacc	cagccacgat	ggatgacatg	gctgtggata	gtgatgagga	1500
ggtggattat	agcaaaatgg	accagggtaa	caagaagggg	cccttaggcc	gttgggactt	1560
tgataccag	gaagaataca	gcgagtatat	gaacaacaaa	gaagctttgc	ccaaggctgc	1620
attccagtat	ggtatcaaaa	tgtctgaagg	gcggaaaacc	aggcgcttca	aggaaaccaa	1680
tgacaaagca	gagcttgatc	gccagtggaa	gaagattagt	gcaatcattg	angaagagga	1740
agaagatgga	agctgatggg	gttgaagtca	aaagacccaa	ataactaatca	ctagttacaa	1800
ccagagatgc	tccacaagga	tatgctcccc	actgttttct	ttctacaatt	tccaaagggtt	1860
gcaagatgtt	tttttgtgat	gaatataaaa	ttttattgtg	taattacttg	gttccattaa	1920
aattggttaa	cttgctaaaa	aaaaaa				1946

<210> 6

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(912)

<220>

<221> misc\_feature

<222> (1)...(915)

<223> n = A,T,C or G

<400> 6

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Met	Met	Ser	Met	Leu	Thr	Gln	Ile	Ser	Pro	Pro	Leu	Leu	Ser	Arg	Ser	
1				5				10						15		
aag	gct	gat	tgc	ccc	acc	atg	gag	gcc	cag	acc	aca	ctg	acc	aca	aat	96
Lys	Ala	Asp	Cys	Pro	Thr	Met	Glu	Ala	Gln	Thr	Thr	Leu	Thr	Thr	Asn	
			20				25					30				
gac	att	gtc	att	agc	aag	ctg	acc	cag	atc	ctt	tca	tac	ctg	agg	cag	144
Asp	Ile	Val	Ile	Ser	Lys	Leu	Thr	Gln	Ile	Leu	Ser	Tyr	Leu	Arg	Gln	
		35				40					45					
gga	acc	cgt	aac	aag	aag	ctt	aag	aag	aag	gat	aaa	ggg	aag	ccg	gaa	192
Gly	Thr	Arg	Asn	Lys	Lys	Leu	Lys	Lys	Lys	Asp	Lys	Gly	Lys	Pro	Glu	
	50					55				60						

gag aag aaa cct cct gag gct gac atg aat att ttt gaa gac att ggg Glu Lys Lys Pro Pro Glu Ala Asp Met Asn Ile Phe Glu Asp Ile Gly 65 70 75 80	240
gat tac gta ccc tcc aca acc aag aca cct cgg gac aag gag cgg gag Asp Tyr Val Pro Ser Thr Thr Lys Thr Pro Arg Asp Lys Glu Arg Glu 85 90 95	288
aga tat cgg gaa cgg gag cgt gat cgg gaa aga gac aga gac cgt gac Arg Tyr Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Asp 100 105 110	336
cga gag cga gag cga gaa cga gat cgg gaa cga gag cga gag cgg gac Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Asp 115 120 125	384
cga gag aga gaa gag gaa aag aag aga cac agc tac ttt gag aag cca Arg Glu Arg Glu Glu Glu Lys Lys Arg His Ser Tyr Phe Glu Lys Pro 130 135 140	432
aaa gta gat gat gag ccc atg gac gtt gac aaa gga cct ggg tct acc Lys Val Asp Asp Glu Pro Met Asp Val Asp Lys Gly Pro Gly Ser Thr 145 150 155 160	480
aag gag ttg atc aag tcc atc aat gaa aag ttt gct ggg tct gct ggc Lys Glu Leu Ile Lys Ser Ile Asn Glu Lys Phe Ala Gly Ser Ala Gly 165 170 175	528
tgg gaa ggc aca gaa tcg ctg aag aag cca gaa gac aaa aag cag ctg Trp Glu Gly Thr Glu Ser Leu Lys Lys Pro Glu Asp Lys Lys Gln Leu 180 185 190	576
gga gat ttc ttt ggc atg tcc aac agt tat gca gag tgc tac cca gcc Gly Asp Phe Phe Gly Met Ser Asn Ser Tyr Ala Glu Cys Tyr Pro Ala 195 200 205	624
acg atg gat gac atg gct gtg gat agt gat gag gag gtg gat tat agc Thr Met Asp Asp Met Ala Val Asp Ser Asp Glu Glu Val Asp Tyr Ser 210 215 220	672
aaa atg gac cag ggt aac aag aag ggg ccc tta ggc cgt tgg gac ttt Lys Met Asp Gln Gly Asn Lys Lys Gly Pro Leu Gly Arg Trp Asp Phe 225 230 235 240	720
gat acc cag gaa gaa tac agc gag tat atg aac aac aaa gaa gct ttg Asp Thr Gln Glu Glu Tyr Ser Glu Tyr Met Asn Asn Lys Glu Ala Leu 245 250 255	768
ccc aag gct gca ttc cag tat ggt atc aaa atg tct gaa ggg cgg aaa Pro Lys Ala Ala Phe Gln Tyr Gly Ile Lys Met Ser Glu Gly Arg Lys 260 265 270	816
acc agg cgc ttc aag gaa acc aat gac aaa gca gag ctt gat cgc cag Thr Arg Arg Phe Lys Glu Thr Asn Asp Lys Ala Glu Leu Asp Arg Gln 275 280 285	864

tgg aag aag att agt gca atc att gan gaa gag gaa gaa gat gga agc 912  
 Trp Lys Lys Ile Ser Ala Ile Ile Xaa Glu Glu Glu Glu Asp Gly Ser  
 290 295 300

tga 915

<210> 7  
 <211> 304  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> VARIANT  
 <222> (1)...(304)  
 <223> Xaa = Any Amino Acid

<400> 7  
 Met Met Ser Met Leu Thr Gln Ile Ser Pro Pro Leu Leu Ser Arg Ser  
 1 5 10 15  
 Lys Ala Asp Cys Pro Thr Met Glu Ala Gln Thr Thr Leu Thr Thr Asn  
 20 25 30  
 Asp Ile Val Ile Ser Lys Leu Thr Gln Ile Leu Ser Tyr Leu Arg Gln  
 35 40 45  
 Gly Thr Arg Asn Lys Lys Leu Lys Lys Lys Asp Lys Gly Lys Pro Glu  
 50 55 60  
 Glu Lys Lys Pro Pro Glu Ala Asp Met Asn Ile Phe Glu Asp Ile Gly  
 65 70 75 80  
 Asp Tyr Val Pro Ser Thr Thr Lys Thr Pro Arg Asp Lys Glu Arg Glu  
 85 90 95  
 Arg Tyr Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Asp  
 100 105 110  
 Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Asp  
 115 120 125  
 Arg Glu Arg Glu Glu Glu Lys Lys Arg His Ser Tyr Phe Glu Lys Pro  
 130 135 140  
 Lys Val Asp Asp Glu Pro Met Asp Val Asp Lys Gly Pro Gly Ser Thr  
 145 150 155 160  
 Lys Glu Leu Ile Lys Ser Ile Asn Glu Lys Phe Ala Gly Ser Ala Gly  
 165 170 175  
 Trp Glu Gly Thr Glu Ser Leu Lys Lys Pro Glu Asp Lys Lys Gln Leu  
 180 185 190  
 Gly Asp Phe Phe Gly Met Ser Asn Ser Tyr Ala Glu Cys Tyr Pro Ala  
 195 200 205  
 Thr Met Asp Asp Met Ala Val Asp Ser Asp Glu Glu Val Asp Tyr Ser  
 210 215 220  
 Lys Met Asp Gln Gly Asn Lys Lys Gly Pro Leu Gly Arg Trp Asp Phe  
 225 230 235 240  
 Asp Thr Gln Glu Glu Tyr Ser Glu Tyr Met Asn Asn Lys Glu Ala Leu  
 245 250 255  
 Pro Lys Ala Ala Phe Gln Tyr Gly Ile Lys Met Ser Glu Gly Arg Lys  
 260 265 270  
 Thr Arg Arg Phe Lys Glu Thr Asn Asp Lys Ala Glu Leu Asp Arg Gln  
 275 280 285  
 Trp Lys Lys Ile Ser Ala Ile Ile Xaa Glu Glu Glu Glu Asp Gly Ser  
 290 295 300

<210> 8

<211> 16,  
<212> PRT  
<213> Homo sapiens

<400> 8  
Arg Arg Gln Thr Leu Ser His Gly Ser Ser Ser Pro Ala Arg Ala Cys  
1 5 10 15